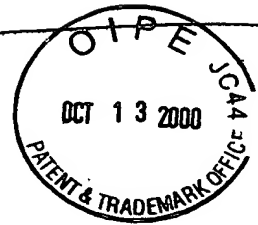


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Howley, Peter M.

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<211> 779

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 2

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      20              25              30

```

```

Thr Ala Leu Val Thr Ala Ala Gly Thr His Arg Asn Ser Ser Thr Ala
      35              40              45

```

```

Lys Thr Val Glu Thr Glu Asp Gly Glu Glu Asp Ile Asp Glu Tyr Gln
      50              55              60

```

```

Arg Lys Arg Ala Ala Gly Ser Gly Glu Ser Thr Pro Glu Arg Ser Asp
      65              70              75              80

```

```

Phe Lys Arg Val Lys His Asp Asn His Lys Thr Leu His Pro Val Asn
      85              90              95

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```

Leu Gln Asn Thr Gly Ala Ala Ser Val Asp Asn Asp Gly Leu His Asn
      100             105             110

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```

Leu Thr Asp Ile Ser Asn Asp Ala Glu Lys Leu Leu Met Ser Val Asp
      115             120             125

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Asp Gly Ser Ala Ala Pro Ser Thr Leu Ser Val Asn Met Gly Val Ala
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Ser His Asn Val Ala Ala Pro Thr Thr Val Asn Ala Ala Thr Ile Thr
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Gly Ser Asp Val Ser Asn Asn Val Asn Ser Ala Thr Ile Asn Asn Pro
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Met Glu Glu Gly Ala Leu Pro Leu Ser Pro Thr Ala Ser Ser Pro Gly
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 Tyr Leu Ser Asp Glu Ile Phe Ser Ala Ile Asn Asn Asn Leu Pro His  
 225 230 235 240  
 Ala Tyr Phe Lys Asn Leu Leu Phe Arg Leu Val Ala Asn Met Asp Arg  
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 Ser Glu Leu Ser Asp Leu Gly Thr Leu Ile Lys Asp Asn Leu Lys Arg  
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 450 455 460  
 Thr Val Arg Cys Leu Asp Ile Val Glu Tyr Lys Asn Ile Lys Tyr Ile  
 465 470 475 480  
 Val Thr Gly Ser Arg Asp Asn Thr Leu His Val Trp Lys Leu Pro Lys  
 485 490 495

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 Phe His Thr Pro Glu Glu Asn Pro Tyr Phe Val Gly Val Leu Arg Gly  
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 Lys Cys Leu Tyr Ile Leu Ser Gly His Thr Asp Arg Ile Tyr Ser Thr  
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 Ile Tyr Asp His Glu Arg Lys Arg Cys Ile Ser Ala Ser Met Asp Thr  
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 Ser Tyr Ala Thr Asn Ser Ala Ser Pro Cys Ala Lys Ile Leu Gly Ala  
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&lt;213&gt; Homo sapiens

&lt;400&gt; 3

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&lt;210&gt; 4

&lt;211&gt; 569

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 4

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      20                      25                      30

Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn Ser Cys Ala
      35                      40                      45

Arg Leu Cys Leu Asn Gln Glu Thr Val Cys Leu Ala Ser Thr Ala Met
      50                      55                      60

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1  
ant

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 Glu Lys Glu Leu Cys Val Lys Tyr Phe Glu Gln Trp Ser Glu Ser Asp  
 100 105 110  
 Gln Val Glu Phe Val Glu His Leu Ile Ser Gln Met Cys His Tyr Gln  
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P 31

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A!  
 Cont

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&lt;210&gt; 8

&lt;211&gt; 640

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*a1  
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 35 40 45  
 Asp Asp Leu Ala Gln Gly Ser Ser Gly Lys Lys Lys Met Thr Met Ala  
 50 55 60  
 Thr Arg Ser Pro Ser Ser Ser Pro Asp Leu Ala Thr Asn Asp Ser Gly  
 65 70 75 80  
 Thr Arg Val Gln Pro Leu Pro Glu Tyr Asn Phe Thr Lys Phe Cys Tyr  
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 Arg His Asn Pro Asp Ile Gln Phe Ser Pro Thr His Thr Ala Cys Tyr  
 100 105 110  
 Lys Gln Asp Leu Lys Arg Thr Gln Glu Ile Asn Ala Asn Ile Ala Lys  
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 Leu Pro Leu Gln Glu Gln Ser Asp Ile His His Ile Ile Ser Lys Tyr  
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 Ser Thr Ser Cys Phe Pro Gln Leu Ser Tyr Ile Ser Ser Leu Val Thr  
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 Arg Val Cys Arg Lys Trp Gln Lys Leu Ala Asp Asp Asp Arg Val Trp  
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 Tyr His Met Cys Glu Gln His Ile Asp Arg Lys Cys Pro Asn Cys Gly  
 225 230 235 240  
 Trp Gly Leu Pro Leu Leu His Met Lys Arg Ala Arg Ile Gln Gln Asn  
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 Ser Thr Gly Ser Ser Ser Asn Ala Asp Ile Gln Thr Gln Thr Thr Arg  
 260 265 270  
 Pro Trp Lys Val Ile Tyr Arg Glu Arg Phe Lys Val Glu Ser Asn Trp  
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 Arg Lys Gly His Cys Arg Ile Gln Glu Phe Lys Gly His Met Asp Gly  
 290 295 300

Ant.  
 Ant.

Val Leu Thr Leu Gln Phe Asn Tyr Arg Leu Leu Phe Thr Gly Ser Tyr  
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 Tyr Ile Thr Gly Glu Cys Ile Ser Thr Tyr Arg Gly His Ser Asp Ser  
 370 375 380  
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 Asp Lys Thr Val Lys Val Trp His Val Glu Ser Arg Thr Cys Tyr Thr  
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 485 490 495  
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 Gly Leu Asp Asn Thr Ile Lys Leu Trp Asp Val Lys Thr Gly Lys Cys  
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 Asp Asn Phe Arg Ile Ile Ser Gly Ser His Asp Gly Ser Ile Lys Val  
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 Trp Asp Leu Gln Ser Gly Lys Cys Met His Thr Phe Asn Gly Arg Arg  
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 Leu Gln Arg Glu Thr Gln His Thr Gln Thr Gln Ser Leu Gly Asp Lys  
 595 600 605

a1  
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<211> 2112

<212> DNA

<213> *Saccharomyces cerevisiae*

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<210> 10

<211> 703

<212> PRT

<213> *Saccharomyces cerevisiae*

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Ser	Phe	Asp	Pro	Gln	Val	Phe	Pro	Ser	Ser	Leu	Ile	His	Gly	Asp	Asn
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Leu	Leu	Pro	Gln	Asp	Asp	Gln	Ile	Ala	Ser	Asp	Pro	Arg	Ser	Glu	Ser
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Asn	Ser	Cys	Asn	Gly	Asn	Thr	Ser	Ser	Ser	Leu	Pro	Cys	Thr	Asp	Ser
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Tyr	Gln	Tyr	Pro	Leu	Lys	His	Ser	Cys	Thr	Pro	Ser	Phe	Leu	Arg	Lys
				85					90					95	
Phe	Asn	Glu	Ser	Ile	Glu	Asn	Val	Ser	Tyr	Lys	Cys	Leu	Asp	His	Ser
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Pro	Pro	Asp	Ser	Val	Pro	Gly	Asp	Phe	Ser	Ile	Ser	Leu	Val	Pro	Gln
		115					120					125			
Arg	Asn	Phe	Leu	Tyr	Ser	His	Ser	Ser	Leu	Pro	Pro	Lys	Ile	Ile	Ser
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Ile	Asp	Arg	Asn	Asn	Arg	Ile	Lys	Leu	Asp	Asn	Ser	Ile	Ser	Ser	Asn
145					150					155					160
Ser	Asp	Asn	Phe	Pro	Pro	Ser	Pro	Lys	Val	Asp	Thr	Ser	Asn	Thr	Val
				165					170					175	
Ser	Pro	Gly	Ser	Lys	Pro	Ile	Ser	Glu	Asp	Leu	Glu	Asp	Leu	Asn	Leu
			180					185					190		
Gln	Ser	Ile	Val	Gln	Thr	Phe	Glu	Asp	Leu	Pro	Glu	Gly	Ile	Gln	Ser
		195					200					205			
Tyr	Ala	Phe	Phe	Gln	Leu	Leu	Arg	Ser	Cys	Asn	Arg	Gln	Ser	Met	Arg
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Leu	Leu	Leu	Asn	Glu	Cys	Glu	Pro	Leu	Leu	Lys	Lys	Asp	Ile	Leu	Ser
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His	Ser	Phe	Leu	Ser	Cys	Arg	Leu	Val	Ser	Pro	Thr	Trp	Asn	Arg	Ile
			260					265					270		
Leu	Asp	Val	His	Thr	Ser	Tyr	Trp	Lys	His	Met	Phe	Ser	Leu	Phe	Gly
		275					280						285		
Phe	Gln	Ile	Asn	Glu	Asn	Asp	Trp	Lys	Tyr	Ala	Asn	Pro	Asn	Leu	Asn
	290					295					300				

al  
ant

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 565 570 575  
 Ser Thr Gly Thr Cys Lys Tyr Val Leu Glu Gly His Asp Ala Phe Val  
 580 585 590  
 Thr Leu Leu Asn Val Phe Gln Asn Arg Leu Ile Ser Gly Ser Ala Asp  
 595 600 605

a!  
 ant



Ser Thr Ile Arg Ile Trp Asp Leu Asn Thr Gly Lys Pro Leu Met Val  
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Leu Pro Ser Asn Ser Gly Tyr Ile Ser Ser Phe Val Ser Asp Glu His  
625 630 635 640

Lys Ile Ile Ser Gly Asn Asp Gly Ser Val Lys Leu Trp Asp Val Arg  
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Thr Gly Lys Leu Leu Arg Phe Leu Leu Thr Asp Leu Thr Lys Ile Trp  
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His Val Asp Phe Asp Ala Met Arg Cys Val Ala Ala Val Gln Arg Asp  
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<211> 2175

<212> DNA

<213> Murine sp.

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Al  
cont

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aaaaaaaaaa aaaaaa                                     2175

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 <213> Murine sp.

<400> 12

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Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn Ser Cys Ala
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Arg Leu Cys Ile Asn Gln Glu Thr Val Cys Leu Thr Ser Thr Ala Met
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Lys Thr Glu Asn Cys Val Ala Lys Ala Lys Leu Ala Asn Gly Thr Ser
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Ser Met Ile Val Pro Lys Gln Arg Lys Leu Ser Ala Ser Tyr Glu Lys
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Glu Lys Glu Leu Cys Val Lys Tyr Phe Glu Gln Trp Ser Glu Ser Asp
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Gln Val Glu Phe Val Glu His Leu Ile Ser Gln Met Cys His Tyr Gln
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```

His Gly His Ile Asn Ser Tyr Leu Lys Pro Met Leu Gln Arg Asp Phe
      130             135             140

```

```

Ile Thr Ala Leu Pro Ala Arg Gly Leu Asp His Ile Ala Glu Asn Ile
      145             150             155             160

```

```

Leu Ser Tyr Leu Asp Ala Lys Ser Leu Cys Ala Ala Glu Leu Val Cys
      165             170             175

```

```

Lys Glu Trp Tyr Arg Val Thr Ser Asp Gly Met Leu Trp Lys Lys Leu
      180             185             190

```

```

Ile Glu Arg Met Val Arg Thr Asp Ser Leu Trp Arg Gly Leu Ala Glu
      195             200             205

```

```

Arg Arg Gly Trp Gly Gln Tyr Leu Phe Lys Asn Lys Pro Pro Asp Glu
      210             215             220

```

```

Asn Ala Pro Pro Asn Ser Phe Tyr Arg Ala Leu Tyr Pro Lys Ile Ile
      225             230             235             240

```

a!  
 cont

Gln Asp Ile Glu Thr Ile Glu Ser Asn Trp Arg Cys Gly Arg His Ser  
 245 250 255  
 Leu Gln Arg Ile His Cys Arg Ser Glu Thr Ser Lys Gly Val Tyr Cys  
 260 265 270  
 Leu Gln Tyr Asp Asp Gln Lys Ile Val Ser Gly Leu Arg Asp Asn Thr  
 275 280 285  
 Ile Lys Ile Trp Asp Lys Ser Thr Leu Glu Cys Lys Arg Ile Leu Thr  
 290 295 300  
 Gly His Thr Gly Ser Val Leu Cys Leu Gln Tyr Asp Glu Arg Val Ile  
 305 310 315 320  
 Ile Thr Gly Ser Ser Asp Ser Thr Val Arg Val Trp Asp Val Asn Ala  
 325 330 335  
 Gly Glu Met Leu Asn Thr Leu Ile His His Cys Glu Ala Val Leu His  
 340 345 350  
 Leu Arg Phe Asn Asn Gly Met Met Val Thr Cys Ser Lys Asp Arg Ser  
 355 360 365  
 Ile Ala Val Trp Asp Met Ala Ser Pro Thr Asp Ile Thr Leu Arg Arg  
 370 375 380  
 Val Leu Val Gly His Arg Ala Ala Val Asn Val Val Asp Phe Asp Asp  
 385 390 395 400  
 Lys Tyr Ile Val Ser Ala Ser Gly Asp Arg Thr Ile Lys Val Trp Asn  
 405 410 415  
 Thr Ser Thr Cys Glu Phe Val Arg Thr Leu Asn Gly His Lys Arg Gly  
 420 425 430  
 Ile Ala Cys Leu Gln Tyr Arg Asp Arg Leu Val Val Ser Gly Ser Ser  
 435 440 445  
 Asp Asn Thr Ile Arg Leu Trp Asp Ile Glu Cys Gly Ala Cys Leu Arg  
 450 455 460  
 Val Leu Glu Gly His Glu Glu Leu Val Arg Cys Ile Arg Phe Asp Asn  
 465 470 475 480  
 Lys Arg Ile Val Ser Gly Ala Tyr Asp Gly Lys Ile Lys Val Trp Asp  
 485 490 495  
 Leu Met Ala Ala Leu Asp Pro Arg Ala Pro Ala Gly Thr Leu Cys Leu  
 500 505 510  
 Arg Thr Leu Val Glu His Ser Gly Arg Val Phe Arg Leu Gln Phe Asp  
 515 520 525  
 Glu Phe Gln Ile Val Ser Ser Ser His Asp Asp Thr Ile Leu Ile Trp  
 530 535 540

a!  
 Cmr

Asp Phe Leu Asn Asp Pro Ala Ala His Ala Glu Pro Pro Arg Ser Pro  
 545 550 555 560

Ser Arg Thr Tyr Thr Tyr Ile Ser Arg  
 565

<210> 13  
 <211> 9  
 <212> PRT  
 <213> Unknown Organism

<220>  
 <223> Description of Unknown Organism: peptide motif

<400> 13  
 Pro Pro Lys Lys Lys Arg Lys Val Ala  
 1 5

<210> 14  
 <211> 32  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: formula  
 sequence

<220>  
 <221> MOD\_RES  
 <222> (3)...(6)  
 <223> any amino acid

<220>  
 <221> MOD\_RES  
 <222> (7)  
 <223> hydrophobic amino acid

<220>  
 <221> MOD\_RES  
 <222> (8)...(9)  
 <223> any amino acid

<220>  
 <221> MOD\_RES  
 <222> (10)  
 <223> hydrophobic amino acid

<220>  
 <221> MOD\_RES  
 <222> (11)  
 <223> any amino acid

<220>  
 <221> MOD\_RES  
 <222> (12)  
 <223> aromatic amino acid

A!  
 Cont

```
<210> 15
<211> 12
<212> PRT
<213> Unknown Organism
```

a' cont

<220>

<223> Description of Unknown Organism: EGF-derived peptide

<400> 15

Cys Met His Ile Glu Ser Leu Asp Ser Tyr Thr Cys  
1 5 10

<210> 16

<211> 12

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: EGF-derived peptide

<400> 16

Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys  
1 5 10

<210> 17

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: formula sequence

<220>

<221> MOD\_RES

<222> (1)

<223> unique amino acid, such as cys or lys

<220>

<221> MOD\_RES

<222> (2)...(3)

<223> amino acid residue selected to modulate the affinity of the internalizing peptide for different membranes

<400> 17

Xaa Xaa Xaa Glu Ala Ala Leu Ala Glu Ala Leu Ala Glu Ala Leu Ala  
1 5 10 15

Glu Ala Leu Ala Glu Ala Leu Ala Glu Ala Leu Glu Ala Leu Ala Ala  
20 25 30

<210> 18

<211> 8

<212> PRT

<213> Unknown Organism

<220>

Al  
any

<223> Description of Unknown Organism: peptide substrate  
for N-myristoyl transferase

<400> 18

Gly Asn Ala Ala Ala Ala Arg Arg  
1 5

<210> 19

<211> 10

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: peptide derived  
from laminin

<400> 19

Cys Asp Pro Gly Tyr Ile Gly Ser Arg Cys  
1 5 10

<210> 20

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nde1-EcoR1 fragment

<400> 20

catatgggtg gctgccgtg cgatatgttc ggttgccgtg ctctccaaa aaagaagaga 60  
aaggtagctg gattc 75

<210> 21

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: RGD/SV40 peptide

<400> 21

Met Gly Gly Cys Arg Gly Asp Met Phe Gly Cys Gly Ala Pro Pro Lys  
1 5 10 15

Lys Lys Arg Lys Val Ala Gly Phe  
20

<210> 22

<211> 225

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nde1-EcoR1 fragment

a!  
ant

<400> 22  
 catatggagc cagtagatcc tagactagag ccctggaagc atccaggaag tcagcctaaa 60  
 actgcttgta ccaattgcta ttgtaaaaag tggtgctttc attgccaagt ttgtttcata 120  
 acaaaagccc ttggcatctc ctatggcagg aagaagcgga gacagcgacg aagacctcct 180  
 caaggcagtc agactcatca agtttctcta agtaagcaag gattc 225

<210> 23  
 <211> 72  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: engineered HIV-1 tat

<400> 23  
 Met Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser  
 1 5 10 15  
 Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe  
 20 25 30  
 His Cys Gln Val Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly  
 35 40 45  
 Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr  
 50 55 60  
 His Gln Val Ser Leu Ser Lys Gln  
 65 70

<210> 24  
 <211> 912  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: NdeI-EcoRI fragment

<400> 24  
 catatgacct ctcgccgctc cgtgaagtcg ggtccgcggg aggttccgcg cgatgagtag 60  
 gaggatctgt actacacccc gtcttcaggt atggcgagtc ccgatagtcc gcctgacacc 120  
 tcccgccgtg gcgccctaca gacacgctcg cgccagaggg gcgaggtccg ttctgctccag 180  
 tacgacgagt cggattatgc cctctacggg ggctcgatcat ccgaagacga cgaacacccg 240  
 gaggtccccc ggacgcggcg tcccgtttcc ggggcggttt tgtccggccc ggggcctgcg 300  
 cgggcgcctc cgccacccgc tgggtccgga ggggcgggac gcacacccac caccgcccc 360  
 cgggcccccc gaaccacgcg ggtggcgact aaggcccccg cggccccggc ggcggagacc 420  
 acccgcggca ggaaatcggc ccagccagaa tccgcgcgac tcccagacgc ccccgcgctc 480  
 acggcgccaa cccgatccaa gacacccgcg caggggctgg ccgaaaagct gcactttagc 540  
 accgcccccc caaacccgca cgcgcatagg accccccggg tggccggctt taacaagcgc 600  
 gtcttctgcg ccgcggtcgg gcgcctggcg gccatgcatg cccggatggc ggcgggtccag 660  
 ctctgggaca tgtcgcgctc gcgcacagac gaagacctca acgaactcct tggcatcacc 720  
 accatccgcg tgacggtctg cgagggcaaa aacctgcttc agcgcgccaa cgagttggtg 780  
 aatccagacg tgggtgcagga cgtcgacgcg gccacggcga ctcgagggcg ttctgcggcg 840  
 tcgcgcccc aagagcgacc tcgagcccc gcccgcctcg cttctcgccc cagacggccc 900  
 gtcgaggaat tc 912

Q1  
 cont.



<210> 25  
 <211> 301  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: engineered HSV-1 VP22

<400> 25

Met Thr Ser Arg Arg Ser Val Lys Ser Gly Pro Arg Glu Val Pro Arg  
 1 5 10 15

Asp Glu Tyr Glu Asp Leu Tyr Tyr Thr Pro Ser Ser Gly Met Ala Ser  
 20 25 30

Pro Asp Ser Pro Pro Asp Thr Ser Arg Arg Gly Ala Leu Gln Thr Arg  
 35 40 45

Ser Arg Gln Arg Gly Glu Val Arg Phe Val Gln Tyr Asp Glu Ser Asp  
 50 55 60

Tyr Ala Leu Tyr Gly Gly Ser Ser Ser Glu Asp Asp Glu His Pro Glu  
 65 70 75 80

Val Pro Arg Thr Arg Arg Pro Val Ser Gly Ala Val Leu Ser Gly Pro  
 85 90 95

Gly Pro Ala Arg Ala Pro Pro Pro Pro Ala Gly Ser Gly Gly Ala Gly  
 100 105 110

Arg Thr Pro Thr Thr Ala Pro Arg Ala Pro Arg Thr Gly Arg Val Ala  
 115 120 125

Thr Lys Ala Pro Ala Ala Pro Ala Ala Glu Thr Thr Arg Gly Arg Lys  
 130 135 140

Ser Ala Gln Pro Glu Ser Ala Ala Leu Pro Asp Ala Pro Ala Ser Thr  
 145 150 155 160

Ala Pro Thr Arg Ser Lys Thr Pro Ala Gln Gly Leu Ala Arg Lys Leu  
 165 170 175

His Phe Ser Thr Ala Pro Pro Asn Pro Asp Ala Pro Trp Thr Pro Arg  
 180 185 190

Val Ala Gly Phe Asn Lys Arg Val Phe Cys Ala Ala Val Gly Arg Leu  
 195 200 205

Ala Ala Met His Ala Arg Met Ala Ala Val Gln Leu Trp Asp Met Ser  
 210 215 220

Arg Pro Arg Thr Asp Glu Asp Leu Asn Glu Leu Leu Gly Ile Thr Thr  
 225 230 235 240

Ile Arg Val Thr Val Cys Glu Gly Lys Asn Leu Leu Gln Arg Ala Asn  
 245 250 255

al  
 cont

Glu Leu Val Asn Pro Asp Val Val Gln Asp Val Asp Ala Ala Thr Ala  
                   260                                  265                                  270

Thr Arg Gly Arg Ser Ala Ala Ser Arg Pro Thr Glu Arg Pro Arg Ala  
                   275                                  280                                  285

Pro Ala Arg Ser Ala Ser Arg Pro Arg Arg Pro Val Glu  
                   290                                  295                                  300

<210> 26  
 <211> 120  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Nde1-EcoR1 fragment

<400> 26  
 catatggacg tcgacgcggc cacggcgact cgagggcggt ctgcggcgtc gcgccccacc 60  
 gagcgacctc gagccccagc ccgctccgct tctcgcccca gacggcccgt cgaggaattc 120

<210> 27  
 <211> 37  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: VP22 (C-terminal domain)

<400> 27  
 Met Asp Val Asp Ala Ala Thr Ala Thr Arg Gly Arg Ser Ala Ala Ser  
   1                                  5                                  10                                  15  
 Arg Pro Thr Glu Arg Pro Arg Ala Pro Ala Arg Ser Ala Ser Arg Pro  
                   20                                  25                                  30  
 Arg Arg Pro Val Glu  
                   35

<210> 28  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: synthetic or  
                   natural linker

<400> 28  
 Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser  
   1                                  5                                  10                                  15

ant

<210> 29  
 <211> 4  
 <212> PRT  
 <213> Unknown Organism

<220>  
 <223> Description of Unknown Organism: tetrapeptide  
 isostere

<400> 29  
 Ala Ile Tyr Tyr  
 1

<210> 30  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 30  
 gcggatccac catggataam aaagagggac ctaataac 38

<210> 31  
 <211> 76  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 31  
 gcgcggccgc ctactcatca tcactagatg gcamcttctg agcaaaacag ccctctggta 60  
 ttatagttgt cctcgt 76

<210> 32  
 <211> 72  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 32  
 cgcgccgcc tactcatcat cactagatgg camttgagcc aaagttttct ctggtattat 60  
 agttgtcctc gt 72

<210> 33  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>

21  
 cont.

<221> modified\_base  
 <222> (20)  
 <223> i

<220>  
 <223> Description of Artificial Sequence: primer

<400> 33  
 gcwatccacc atggataatn taaagaggga cctaataac 39

<210> 34  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 34  
 gtaggtgtat ctccatgtgg tatratagtr gtcc 34

<210> 35  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 35  
 ggacaactat aataccacat ggagatacac ctac 34

<210> 36  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 36  
 gcctcgagtc actcctcctc tgagctgtc 29

<210> 37  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 37  
 gcggatccac catggataam aaagaggac ctaataac 38

a!  
 Cont

<210> 38  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 38  
 cctatcacat ctatatttta ttggtattat agttgtc 37

<210> 39  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 39  
 gacaactata ataccaataa aatatagatg tgatagg 37

<210> 40  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 40  
 gcctcgagtc ataatgtgtt agtatattgt cctg 34

<210> 41  
 <211> 69  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 41  
 gcggatccac catggaggaa gaagagtata tgcccatgga ggagactctt tgccaacggt 60  
 ttaaattgtg 69

<210> 42  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

a!  
 cont

<400> 42  
gcgcggccgc tcatatagac ataatccag tagac 35

<210> 43  
<211> 65  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 43  
gcggatccgc caccatggac tacaaggacg acgatgacaa agatgaccg gccgaggcgg 60  
tgctg 65

<210> 44  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 44  
gtaggtgtat ctccatgtct ggagatgtag gtgtatg 37

<210> 45  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 45  
catacaccta catctccaga catggagata cacctac 37

<210> 46  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 46  
gcgcggccgc tcactcctcc tctgagctgt c 31

<210> 47  
<211> 5  
<212> PRT  
<213> Unknown Organism

al  
cont

a'  
ant

<220>

<223> Description of Unknown Organism: LFCSE motif

<400> 47

Leu Phe Cys Ser Glu

1

5

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